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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/828,307A

DATE: 08/08/2001
TIME: 14:38:55

Input Set : A:\ES.txt
Output Set: N:\CRF3\08082001\I828307A.raw

3 <110> APPLICANT: Mack, David
4 Gish, Kurt
5 Wilson, Keith
7 <120> TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSING CANCER, COMPOSITIONS, AND
METHODS OF

8 SCREENING FOR CANCER MODULATORS
10 <130> FILE REFERENCE: A-69192-1/DJB/JJD/AMS
OK C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/828,307A
OK C--> 12 <141> CURRENT FILING DATE: 2001-04-06
12 <150> PRIOR APPLICATION NUMBER: US 09/608,821
13 <151> PRIOR FILING DATE: 2000-06-30
15 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3794
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (38)..(2635)
28 <400> SEQUENCE: 1

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31                                     1           5
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34 Ser Leu Leu Leu Leu Gly Leu Cys Gly Asn Ser Phe Ser Gly Gly Gln
35          10           15           20
37 cct tca tcc aca gat gct cct aag gct tgg aat tat gaa ttg cct gca      151
38 Pro Ser Ser Thr Asp Ala Pro Lys Ala Trp Asn Tyr Glu Leu Pro Ala
39          25           30           35
41 aca aat tat gag acc caa gac tcc cat aaa gct gga ccc att ggc att      199
42 Thr Asn Tyr Glu Thr Gln Asp Ser His Lys Ala Gly Pro Ile Gly Ile
43          40           45           50
45 ctc ttt gaa cta gtg cat atc ttt ctc tat gtg gta cag ccg cgt gat      247
46 Leu Phe Glu Leu Val His Ile Phe Leu Tyr Val Val Gln Pro Arg Asp
47 55          60           65           70
49 ttc cca gaa gat act ttg aga aaa ttc tta cag aag gca tat gaa tcc      295
50 Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu Gln Lys Ala Tyr Glu Ser
51          75           80           85
53 aaa att gat tat gac aag cca gaa act gta atc tta ggt cta aag att      343
54 Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val Ile Leu Gly Leu Lys Ile
55          90           95           100
57 gtc tac tat gaa gca ggg att att cta tgc tgt gtc ctg ggg ctg ctg      391
58 Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys Cys Val Leu Gly Leu Leu
59          105          110          115
61 ttt att att ctg atg cct ctg gtg ggg tat ttc ttt tgt atg tgt cgt      439
62 Phe Ile Ile Leu Met Pro Leu Val Gly Tyr Phe Phe Cys Met Cys Arg
63          120          125          130

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66	Cys	Cys	Asn	Lys	Cys	Gly	Gly	Glu	Met	His	Gln	Arg	Gln	Lys	Glu	Asn	
67	135					140					145					150	
69	ggg	ccc	ttc	ctg	agg	aaa	tgc	ttt	gca	atc	tcc	ctg	ttg	gtg	att	tgt	535
70	Gly	Pro	Phe	Leu	Arg	Lys	Cys	Phe	Ala	Ile	Ser	Leu	Leu	Val	Ile	Cys	
71						155					160					165	
73	ata	ata	ata	agc	att	ggc	atc	ttc	tat	ggt	ttt	gtg	gca	aat	cac	cag	583
74	Ile	Ile	Ile	Ser	Ile	Gly	Ile	Phe	Tyr	Gly	Phe	Val	Ala	Asn	His	Gln	
75						170					175					180	
77	gta	aga	acc	cgg	atc	aaa	agg	agt	cgg	aaa	ctg	gca	gat	agc	aat	ttc	631
78	Val	Arg	Thr	Arg	Ile	Lys	Arg	Ser	Arg	Lys	Leu	Ala	Asp	Ser	Asn	Phe	
79						185					190					195	
81	aag	gac	ttg	cga	act	ctc	ttg	aat	gaa	act	cca	gag	caa	atc	aaa	tat	679
82	Lys	Asp	Leu	Arg	Thr	Leu	Leu	Asn	Glu	Thr	Pro	Glu	Gln	Ile	Lys	Tyr	
83						200					205					210	
85	ata	ttg	gcc	cag	tac	aac	act	acc	aag	gac	aag	gcg	ttc	aca	gat	ctg	727
86	Ile	Leu	Ala	Gln	Tyr	Asn	Thr	Thr	Lys	Asp	Lys	Ala	Phe	Thr	Asp	Leu	
87	215					220					225					230	
89	aac	agt	atc	aat	tca	gtg	cta	gga	ggc	gga	att	ctt	gac	cga	ctg	aga	775
90	Asn	Ser	Ile	Asn	Ser	Val	Leu	Gly	Gly	Ile	Leu	Asp	Arg	Leu	Arg		
91						235					240					245	
93	ccc	aac	atc	atc	cct	gtt	ctt	gat	gag	att	aag	tcc	atg	gca	aca	gcg	823
94	Pro	Asn	Ile	Ile	Pro	Val	Leu	Asp	Glu	Ile	Lys	Ser	Met	Ala	Thr	Ala	
95						250					255					260	
97	atc	aag	gag	acc	aaa	gag	gcg	ttg	gag	aac	atg	aac	agc	acc	ttg	aag	871
98	Ile	Lys	Glu	Thr	Lys	Glu	Ala	Leu	Glu	Asn	Met	Asn	Ser	Thr	Leu	Lys	
99						265					270					275	
101	agc	ttg	cac	caa	caa	agt	aca	cag	ctt	agc	agc	agt	ctg	acc	agc	gtg	919
102	Ser	Leu	His	Gln	Gln	Ser	Thr	Gln	Leu	Ser	Ser	Ser	Leu	Thr	Ser	Val	
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105	aaa	act	agc	ctg	cgg	tca	tct	ctc	aat	gac	cct	ctg	tgc	ttg	gtg	cat	967
106	Lys	Thr	Ser	Leu	Arg	Ser	Ser	Leu	Asn	Asp	Pro	Leu	Cys	Leu	Val	His	
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109	cca	tca	agt	gaa	acc	tgc	aac	agc	atc	aga	ttg	tct	cta	agc	cag	ctg	1015
110	Pro	Ser	Ser	Glu	Thr	Cys	Asn	Ser	Ile	Arg	Leu	Ser	Leu	Ser	Gln	Leu	
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113	aat	agc	aac	cct	gaa	ctg	agg	cag	ctt	cca	ccc	gtg	gat	gca	gaa	ctt	1063
114	Asn	Ser	Asn	Pro	Glu	Leu	Arg	Gln	Leu	Pro	Pro	Val	Asp	Ala	Glu	Leu	
115						330					335					340	
117	gac	aac	gtt	aat	aac	gtt	ctt	agg	aca	gat	ttg	gat	ggc	ctg	gtc	caa	1111
118	Asp	Asn	Val	Asn	Asn	Val	Leu	Arg	Thr	Asp	Leu	Asp	Gly	Leu	Val	Gln	
119						345					350					355	
121	cag	ggc	tat	caa	tcc	ctt	aat	gat	ata	cct	gac	aga	gta	caa	cgc	caa	1159
122	Gln	Gly	Tyr	Gln	Ser	Leu	Asn	Asp	Ile	Pro	Asp	Arg	Val	Gln	Arg	Gln	
123						360					365					370	
125	acc	acg	act	gtc	gta	gca	ggt	atc	aaa	agg	gtc	ttg	aat	tcc	att	ggt	1207
126	Thr	Thr	Thr	Val	Val	Ala	Gly	Ile	Lys	Arg	Val	Leu	Asn	Ser	Ile	Gly	
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129	tca	gat	atc	gac	aat	gta	act	cag	cgt	ctt	cct	att	cag	gat	ata	ctc	1255

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134	Ser	Ala	Phe	Ser	Val	Tyr	Val	Asn	Asn	Thr	Glu	Ser	Tyr	Ile	His	Arg	
135				410					415					420			
137	aat	tta	cct	aca	ttg	gaa	gag	tat	gat	tca	tac	tgg	tgg	ctg	ggt	ggc	1351
138	Asn	Leu	Pro	Thr	Leu	Glu	Glu	Tyr	Asp	Ser	Tyr	Trp	Trp	Leu	Gly	Gly	
139			425					430						435			
141	ctg	gtc	atc	tgc	tct	ctg	ctg	acc	ctc	atc	gtg	att	ttt	tac	tac	ctg	1399
142	Leu	Val	Ile	Cys	Ser	Leu	Leu	Thr	Leu	Ile	Val	Ile	Phe	Tyr	Tyr	Leu	
143		440						445						450			
145	ggc	tta	ctg	tgt	ggc	gtg	tgc	ggc	tat	gac	agg	cat	gcc	acc	ccg	acc	1447
146	Gly	Leu	Leu	Cys	Gly	Val	Cys	Gly	Tyr	Asp	Arg	His	Ala	Thr	Pro	Thr	
147	455					460					465					470	
149	acc	cga	ggc	tgt	gtc	tcc	aac	acc	gga	ggc	gtc	ttc	ctc	atg	ggt	gga	1495
150	Thr	Arg	Gly	Cys	Val	Ser	Asn	Thr	Gly	Gly	Val	Phe	Leu	Met	Val	Gly	
151				475						480					485		
153	ggt	gga	tta	agt	ttc	ctc	ttt	tgc	tgg	ata	ttg	atg	atc	att	gtg	ggt	1543
154	Val	Gly	Leu	Ser	Phe	Leu	Phe	Cys	Trp	Ile	Leu	Met	Ile	Ile	Val	Val	
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158	Leu	Thr	Phe	Val	Phe	Gly	Ala	Asn	Val	Glu	Lys	Leu	Ile	Cys	Glu	Pro	
159			505					510						515			
161	tac	acg	agc	aag	gaa	tta	ttc	cgg	ggt	ttg	gat	aca	ccc	tac	tta	cta	1639
162	Tyr	Thr	Ser	Lys	Glu	Leu	Phe	Arg	Val	Leu	Asp	Thr	Pro	Tyr	Leu	Leu	
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165	aat	gaa	gac	tgg	gaa	tac	tat	ctc	tct	ggg	aag	cta	ttt	aat	aaa	tca	1687
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171				555						560					565		
173	aga	ggc	act	tac	ggc	act	ctt	cac	ctg	cag	aac	agc	ttc	aat	atc	agt	1783
174	Arg	Gly	Thr	Tyr	Gly	Thr	Leu	His	Leu	Gln	Asn	Ser	Phe	Asn	Ile	Ser	
175			570						575					580			
177	gaa	cat	ctc	aac	att	aat	gag	cat	act	gga	agc	ata	agc	agt	gaa	ttg	1831
178	Glu	His	Leu	Asn	Ile	Asn	Glu	His	Thr	Gly	Ser	Ile	Ser	Ser	Glu	Leu	
179			585					590						595			
181	gaa	agt	ctg	aag	gta	aat	ctt	aat	atc	ttt	ctg	ttg	ggt	gca	gca	gga	1879
182	Glu	Ser	Leu	Lys	Val	Asn	Leu	Asn	Ile	Phe	Leu	Leu	Gly	Ala	Ala	Gly	
183		600					605							610			
185	aga	aaa	aac	ctt	cag	gat	ttt	gct	gct	tgt	gga	ata	gac	aga	atg	aat	1927
186	Arg	Lys	Asn	Leu	Gln	Asp	Phe	Ala	Ala	Cys	Gly	Ile	Asp	Arg	Met	Asn	
187	615					620					625					630	
189	tat	gac	agc	tac	ttg	gct	cag	act	ggt	aaa	tcc	ccc	gca	gga	gtg	aat	1975
190	Tyr	Asp	Ser	Tyr	Leu	Ala	Gln	Thr	Gly	Lys	Ser	Pro	Ala	Gly	Val	Asn	
191				635						640					645		
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198 Pro Gly Asn Leu Arg Asn Ser Leu Lys Arg Asp Ala Gln Thr Ile Lys				
199	665	670	675	
201 aca att cac cag caa cga gtc ctt cct ata gaa caa tca ctg agc act	2119			
202 Thr Ile His Gln Gln Arg Val Leu Pro Ile Glu Gln Ser Leu Ser Thr				
203	680	685	690	
205 cta tac caa agc gtc aag ata ctt caa cgc aca ggg aat gga ttg ttg	2167			
206 Leu Tyr Gln Ser Val Lys Ile Leu Gln Arg Thr Gly Asn Gly Leu Leu				
207 695	700	705	710	
209 gag aga gta act agg att cta gct tct ctg gat ttt gct cag aac ttc	2215			
210 Glu Arg Val Thr Arg Ile Leu Ala Ser Leu Asp Phe Ala Gln Asn Phe				
211	715	720	725	
213 atc aca aac aat act tcc tct gtt att att gag gaa act aag aag tat	2263			
214 Ile Thr Asn Asn Thr Ser Ser Val Ile Ile Glu Glu Thr Lys Lys Tyr				
215	730	735	740	
217 ggg aga aca ata ata gga tat ttt gaa cat tat ctg cag tgg atc gag	2311			
218 Gly Arg Thr Ile Ile Gly Tyr Phe Glu His Tyr Leu Gln Trp Ile Glu				
219	745	750	755	
221 ttc tct atc agt gag aaa gtg gca tgc tgc aaa cct gtg gcc acc gct	2359			
222 Phe Ser Ile Ser Glu Lys Val Ala Ser Cys Lys Pro Val Ala Thr Ala				
223	760	765	770	
225 cta gat act gct gtt gat gtc ttt ctg tgt agc tac att atc gac ccc	2407			
226 Leu Asp Thr Ala Val Asp Val Phe Leu Cys Ser Tyr Ile Ile Asp Pro				
227 775	780	785	790	
229 ttg aat ttg ttt tgg ttt ggc ata gga aaa gct act gta ttt tta ctt	2455			
230 Leu Asn Leu Phe Trp Phe Gly Ile Gly Lys Ala Thr Val Phe Leu Leu				
231	795	800	805	
233 ccg gct cta att ttt gcg gta aaa ctg gct aag tac tat cgt cga atg	2503			
234 Pro Ala Leu Ile Phe Ala Val Lys Leu Ala Lys Tyr Tyr Arg Arg Met				
235	810	815	820	
237 gat tcg gag gac gtg tac gat gat gtt gaa act ata ccc atg aaa aat	2551			
238 Asp Ser Glu Asp Val Tyr Asp Asp Val Glu Thr Ile Pro Met Lys Asn				
239	825	830	835	
241 atg gaa aat ggt aat aat ggt tat cat aaa gat cat gta tat ggt att	2599			
242 Met Glu Asn Gly Asn Asn Gly Tyr His Lys Asp His Val Tyr Gly Ile				
243	840	845	850	
245 cac aat cct gtt atg aca agc cca tca caa cat tga tagctgatgt	2645			
246 His Asn Pro Val Met Thr Ser Pro Ser Gln His				
247 855	860	865		
249 tgaaactgct tgagcatcag gatactcaaa gtggaaagga tcacagattt ttggtagttt	2705			
251 ctgggtctac aaggactttc caaatccagg agcaacgccg gtggcaacgt agtgactcag	2765			
253 gcgggcacca aggcaacggc accattgggtc tctgggtagt gctttaagaa tgaacacaat	2825			
255 cacgttatag tccatgggtcc atcactattc aaggatgact ccctcccttc ctgtctattt	2885			
257 ttgtttttta cttttttaca ctgagtttct atttagacac tacaacatat ggggtgtttg	2945			
259 ttcccatgtg atgcatttct atcaaaactc tatcaaatgt gatggctaga ttctaacata	3005			
261 ttgccatgtg tggagtgtgc tgaacacaca ccagtttaca ggaaagatgc attttgtgta	3065			
263 cagtaaaccg tgtatatacc ttttgttacc acagagtttt ttaaacaat gagtattata	3125			
265 ggacttttct ctaaatgagc taaataagtc accattgact tcttggtgct gttgaaaata	3185			

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269 ctattatact ttatcaaaga ttggccatgt tccacttgga aatggcatgc aaaagccatc 3305
271 atagagaaac ctgcgtaact ccacttgaca aattcaaaag agagagagag atcttgagag 3365
273 agaaatgctg ttcgttcaaa agtggagttg ttttaacaga tgccaattac ggtgtacagt 3425
275 ttaacagagt tttctgttgc attaggataa acattaattg gagtgcagct aacatgagta 3485
277 tcatcagact agtatcaagt gttctaaaat gaaatatgag aagatcctgt cacaattctt 3545
279 agatctggtg tccagcatgg atgaaacctt tgagtttggg ccctaaattt gcatgaaagc 3605
281 acaaggtaaa tattcatttg cttcaggagt ttcatgttgg atctgtcatt atcaaaagtg 3665
283 atcagcaatg aagaactggt cggacaaaat ttaacgttga tgtaatggaa ttccagatgt 3725
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292 <212> TYPE: PRT
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302 20 25 30
305 Asn Tyr Glu Leu Pro Ala Thr Asn Tyr Glu Thr Gln Asp Ser His Lys
306 35 40 45
309 Ala Gly Pro Ile Gly Ile Leu Phe Glu Leu Val His Ile Phe Leu Tyr
310 50 55 60
313 Val Val Gln Pro Arg Asp Phe Pro Glu Asp Thr Leu Arg Lys Phe Leu
314 65 70 75 80
317 Gln Lys Ala Tyr Glu Ser Lys Ile Asp Tyr Asp Lys Pro Glu Thr Val
318 85 90 95
321 Ile Leu Gly Leu Lys Ile Val Tyr Tyr Glu Ala Gly Ile Ile Leu Cys
322 100 105 110
325 Cys Val Leu Gly Leu Leu Phe Ile Ile Leu Met Pro Leu Val Gly Tyr
326 115 120 125
329 Phe Phe Cys Met Cys Arg Cys Cys Asn Lys Cys Gly Gly Glu Met His
330 130 135 140
333 Gln Arg Gln Lys Glu Asn Gly Pro Phe Leu Arg Lys Cys Phe Ala Ile
334 145 150 155 160
337 Ser Leu Leu Val Ile Cys Ile Ile Ile Ser Ile Gly Ile Phe Tyr Gly
338 165 170 175
341 Phe Val Ala Asn His Gln Val Arg Thr Arg Ile Lys Arg Ser Arg Lys
342 180 185 190
345 Leu Ala Asp Ser Asn Phe Lys Asp Leu Arg Thr Leu Leu Asn Glu Thr
346 195 200 205
349 Pro Glu Gln Ile Lys Tyr Ile Leu Ala Gln Tyr Asn Thr Thr Lys Asp
350 210 215 220
353 Lys Ala Phe Thr Asp Leu Asn Ser Ile Asn Ser Val Leu Gly Gly Gly
354 225 230 235 240
357 Ile Leu Asp Arg Leu Arg Pro Asn Ile Ile Pro Val Leu Asp Glu Ile
358 245 250 255
361 Lys Ser Met Ala Thr Ala Ile Lys Glu Thr Lys Glu Ala Leu Glu Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/828,307A

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1025 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5